

SEQUENCE LISTING

<110> Kharbanda, Surrender
 Kufe, Donald
 <120> Modulation of Interaction of MUC1 with MUC1 Ligands
 <130> DFCI:005US
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 <141> 2006-04-24
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 <160> 71
 <170> PatentIn version 3.3
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Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly
 20 25 30

Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala
 35 40 45

Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Phe Asn
 50 55 60

Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg
 65 70 75 80

Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu
 85 90 95

Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu
 100 105 110

Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Met Glu Thr
 115 120 125

Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr
 130 135 140

Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln
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Ser Gly Ala Gly

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 atcaatgtcc acgacatgga gacacagttc aatcagtata aaacggaagc agcctctcga 420
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 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp
 50 55 60

Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile
 65 70 75 80

Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro
85 90 95

Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile
100 105 110

Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala
115 120 125

Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val
130 135 140

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145 150 155

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Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser
50 55 60

Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser
65 70 75 80

Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu
85 90 95

Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe
100 105 110

Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
115 120 125

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
130 135 140

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
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caaggggggtt ttctgggcct ctccaatatt aagttcaggc caggatctgt ggtggtacaa 360
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20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Thr
35 40 45

Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln
50 55 60

Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg
65 70 75 80

Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr
85 90 95

Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu
100 105 110

Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp
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130 135 140

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<212> DNA
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cagagaagtt cagtgccag caccgactac taccaagagc tgcagagaga cttttctgaa 180
atgtttttgc agatttataa acaagggggt tttctgggcc tctccaatat taagttcagg 240
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gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 360
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<213> Homo sapiens

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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg
50 55 60

Glu Thr Phe Leu Lys Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu
65 70 75 80

Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe
85 90 95

Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser
100 105 110

Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly
115 120 125

Ala Gly
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<210> 10
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<212> DNA
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cagagaagtt cagtgccag ctctactgag aagaatgcta tcccagcacc gactactacc 180
aagagctgca gagagacatt tctgaaatgg ccaggatctg tgggtgtaca attgactctg 240
gccttccgag aagggtacat caatgtccac gacatggaga cacagttcaa tcagtataaa 300
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Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val
35 40 45

Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val
50 55 60

Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn
65 70 75 80

Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser
85 90 95

Ala Gln Ser Gly Ala Gly
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<210> 12
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<213> Homo sapiens

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20 25 30
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50 55 60
 Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65 70 75 80
 Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85 90 95
 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
 100 105 110
 Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
 115 120 125
 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
 130 135 140
 Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
 145 150 155 160
 Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val His
 165 170 175
 Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu
 180 185 190
 Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys
 195 200 205
 Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr Thr
 210 215 220
 Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser Thr His His Ser
 225 230 235 240
 Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln Leu
 245 250 255
 Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn Leu
 260 265 270
 Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu
 275 280 285
 Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly
 290 295 300

Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val
 305 310 315 320

Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp
 325 330 335

Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr
 340 345 350

Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe
 355 360 365

Ser Ala Gln Ser Gly Ala Gly
 370 375

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 ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 1080
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 <212> PRT
 <213> Homo sapiens

<400> 15

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 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65 70 75 80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85 90 95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
 100 105 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Asn Arg Pro
 115 120 125

Ala Leu Gly Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser
 130 135 140

Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser
 145 150 155 160

Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile
 165 170 175

Pro Ser His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr
 180 185 190

Lys Thr Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr
 195 200 205

Ser Ser Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe
 210 215 220

Phe Phe Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu
 225 230 235 240

Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser
 245 250 255

Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser
 260 265 270

Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala
 275 280 285

Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn
 290 295 300

Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp
 305 310 315 320

Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
 325 330 335

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<210> 16
 <211> 1011
 <212> DNA
 <213> Homo sapiens

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 acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac 960
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<210> 17
 <211> 175
 <212> PRT
 <213> Homo sapiens

<400> 17

Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
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His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
 20 25 30

Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
 35 40 45

Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
 50 55 60

Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
 65 70 75 80

Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
 85 90 95

Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile
 100 105 110

Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg
 115 120 125

Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr
 130 135 140

Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser
 145 150 155 160

Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
 165 170 175

<210> 18
 <211> 525
 <212> DNA
 <213> Homo sapiens

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 ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 480
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<400> 19

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Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala
 20 25 30

Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro
 35 40 45

Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
 50 55

<210> 20
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 <212> DNA
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<210> 21
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 <212> PRT
 <213> Homo sapiens

<400> 21

Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn
1 5 10 15

Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala
20 25 30

Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro
35 40 45

Phe Pro
50

<210> 22
<211> 150
<212> DNA
<213> Homo sapiens

<400> 22
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gacgtcagcg tgagtgatgt gccatttcct 150

<210> 23
<211> 49
<212> PRT
<213> Homo sapiens

<400> 23

Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn
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Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp
20 25 30

Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
35 40 45

Gly

<210> 24
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<212> DNA
<213> Homo sapiens

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cctttctctg cccagtctgg ggctggg 147

<210> 25
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 25

Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn
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 20 25 30

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
 35 40 45

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val
 50 55 60

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His
 65 70 75 80

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg
 85 90 95

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro
 100 105 110

Phe Ser Ala Gln Ser Gly Ala Gly
 115 120

<210> 26
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 <212> DNA
 <213> Homo sapiens

<400> 26

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ccaggatctg tggtggtaca attgactctg gccttccgag aaggtaccat caatgtccac	240
gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg	300
atctcagacg tcagcgtgag tgatgtgcca tttcctttct ctgcccagtc tggggctggg	360

<210> 27
 <211> 77
 <212> PRT
 <213> Homo sapiens

<400> 27

Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg Glu Thr Phe Leu Lys
1 5 10 15

Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
20 25 30

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
35 40 45

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
50 55 60

Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
65 70 75

<210> 28

<211> 231

<212> DNA

<213> Homo sapiens

<400> 28

atcccagcac cgactactac caagagctgc agagagacat ttctgaaatg gccaggatct 60

gtggtgtgtac aattgactct ggccttccga gaaggtacca tcaatgtcca cgacatggag 120

acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac 180

gtcagcgtga gtgatgtgcc atttcctttc tctgcccagt ctggggctgg g 231

<210> 29

<211> 112

<212> PRT

<213> Homo sapiens

<400> 29

Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn
1 5 10 15

Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln
20 25 30

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
35 40 45

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val
50 55 60

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His
65 70 75 80

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg
85 90 95

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro
100 105 110

<210> 30
<211> 336
<212> DNA
<213> Homo sapiens

<400> 30
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tcctctctgg aagatccag caccgactac taccaagagc tgcagagaga catttctgaa 120
atgtttttgc agatttataa acaaggggggt tttctgggcc tctccaatat taagttcagg 180
ccaggatctg tggtggtaca attgactctg gccttccgag aaggtaccat caatgtccac 240
gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 300
atctcagacg tcagcgtgag tgatgtgcca tttcct 336

<210> 31
<211> 66
<212> PRT
<213> Homo sapiens

<400> 31

Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg Glu Thr Phe Leu Lys
1 5 10 15

Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
20 25 30

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
35 40 45

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
50 55 60

Asp Val
65

<210> 32
<211> 198
<212> DNA
<213> Homo sapiens

<400> 32
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gtggtggtac aattgactct ggccttccga gaaggtacca tcaatgtcca cgacatggag 120

acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac 180
 gtcagcgtga gtgatgtg 198

<210> 33
 <211> 232
 <212> PRT
 <213> HS

<400> 33

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 34
 <211> 699
 <212> DNA
 <213> HS

<400> 34
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 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 360
 atctccaaag ccaaaggga gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
 cccgtgctgg actccgtcgg ctctttcttc ctctacagca agctcaccgt ggacaagagc 600
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 tacacgcaga agagcctctc cctgtctccg ggtaaatga 699

<210> 35
 <211> 230
 <212> PRT
 <213> HS

<400> 35

Lys Ser Cys Asp Lys Pro His Thr Cys Pro Leu Cys Pro Ala Pro Glu
 1 5 10 15

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 20 25 30

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 35 40 45

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 50 55 60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 65 70 75 80

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
85 90 95

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
100 105 110

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
115 120 125

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
130 135 140

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
145 150 155 160

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Ala
165 170 175

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
180 185 190

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
195 200 205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
210 215 220

Ser Leu Ser Pro Gly Lys
225 230

<210> 36
<211> 690
<212> DNA
<213> HS

<400> 36
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ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 120
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 180
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 240
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 300
gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 360
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 420
ctgaccaaga accaggtcag cctgacctgc ctagtcaaag gcttctatcc cagcgacatc 480

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaaggccac gcctcccgtg 540
 ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 600
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 660
 cagaagagcc tctccctgtc tccgggtaaa 690

<210> 37
 <211> 228
 <212> PRT
 <213> HS

<400> 37

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
 1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu
 50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
 65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
 85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
 100 105 110

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
 115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 210 215 220

Ser Pro Gly Lys
 225

<210> 38
 <211> 687
 <212> DNA
 <213> HS

<400> 38
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 acgtgcgtgg tgggtggacgt gagccacgaa gaccccagg tccagttcaa ctggtacgtg 180
 gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 240
 ttccgtgtgg tcagcgtcct caccgtcgtg caccaggact ggctgaacgg caaggagtac 300
 aagtgcaagg tctccaacaa aggcctccca gccccatcg agaaaaccat ctccaaaacc 360
 aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 420
 aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 480
 gagtgggaga gcaatgggca gccggagaac aactacaaga ccacacctcc catgctggac 540
 tccgacggct ctttcttctt ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 600
 gggaaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag 660
 agcctctccc tgtctccggg taaatga 687

<210> 39
 <211> 229
 <212> PRT
 <213> Homo Sapiens

<400> 39

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
 1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 40
<211> 690
<212> DNA
<213> HS

<400> 40
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tcagtcttcc tggtccccc aaaaccaag gacactctca tgatctcccg gaccctgag 120
gtcacgtgcg tgggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac 180
gtggatggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc 240
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgar cggcaaggag 300
tacaagtgca aggtctccar caaaggcctc ccgtcctcca tcgagaaaac catctccaam 360

gccamagggc agccccgaga gccacaggtg tacaccctgc ccccatccca ggaggagatg 420
 accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc 480
 gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 540
 gactccgacg gctccttctt cctctacagc aggctaaccg tggacaagag cagktggcag 600
 gaggggaatg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag 660
 aagagcctct ccctgtctct gggtaaatga 690

<210> 41
 <211> 585
 <212> PRT
 <213> HS

<400> 41

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Gln Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Pro Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Met Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
 580 585

<210> 42
 <211> 1758
 <212> DNA
 <213> HS

<400> 42
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 aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa 180
 aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240
 cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300
 tgcttcttgc aacacaaaga tgacaatcca aatctccccc gattggtgag accagaggtt 360
 gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420
 gaaattgccca gaagacatcc ttacttttat gccccgcaac tccttttctt tgctaaaagg 480
 tataaagctg cttttacaga atgttgccaa gctgctgata aagcagcctg cctggttgcca 540

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aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt 600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660
cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720
gtccacacgg aatgctgcc a tggagatctg cttgaatgtg ctgatgacag ggcggacctt 780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840
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gacttgcctt cattagcggc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct 960
gaggcaaagg atgtcttctt gggcatgttt ttgtatgaat atgcaagaag gcatcctgat 1020
tactctgtcg tactgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc 1080
tgtgccgctc cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt 1140
atggaagagc ctcagaattt aatcaaaca aattgtgagc tttttgagca gcttggagag 1200
tacaaattcc agaatgcgct attagtctgt tacaccaaga aagtaccca agtgtcaact 1260
ccaactcttg tagaggtctc aagaaacct a ggaagtggtg gcagcaaata ttgtaaacat 1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta 1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc 1440
ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa 1500
gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560
agacaaatca agaaacaaac tgcacttggt gagcttgtga aacacaagcc caaggcaaca 1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680
gctgacgata aggaaacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740
gctgccttag gcttataa 1758

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<210> 43
<211> 110
<212> PRT
<213> Homo Sapiens

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<400> 43
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Met Arg Phe Met Thr Leu Leu Phe Leu Thr Ala Leu Ala Gly Ala Leu
1           5           10           15

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Val Cys Ala Tyr Asp Pro Glu Ala Ala Ser Ala Pro Gly Ser Gly Asn
          20           25           30

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Pro Cys His Glu Ala Ser Ala Ala Gln Lys Glu Asn Ala Gly Glu Asp
          35           40           45

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Pro Gly Leu Ala Arg Gln Ala Pro Lys Pro Arg Lys Gln Arg Ser Ser
50           55           60

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Leu Leu Glu Lys Gly Leu Asp Gly Ala Lys Lys Ala Val Gly Gly Leu
65 70 75 80

Gly Lys Leu Gly Lys Asp Ala Val Glu Asp Leu Glu Ser Val Gly Lys
85 90 95

Gly Ala Val His Asp Val Lys Asp Val Leu Asp Ser Val Leu
100 105 110

<210> 44
<211> 333
<212> DNA
<213> HS

<400> 44
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gatccagagg ccgcctctgc cccaggatcg gggaaccctt gccatgaagc atcagcagct 120
caaaaggaaa atgcaggtga agaccaggagg ttagccagac aggcaccaa gccaaggaag 180
cagagatcca gccttctgga aaaaggccta gacggagcaa aaaaagctgt ggggggactc 240
ggaaaactag gaaaagatgc agtcgaagat ctagaaagcg tgggtaaagg agccgtccat 300
gacgttaaag acgtccttga ctcagtacta tag 333

<210> 45
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 45
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<210> 46
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 46
aagcatcagc agctcaaaag g 21

<210> 47
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 47
aaaaggaaaa tgcaggtgaa g 21

<210> 48
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 48
aaaggaaaat gcaggtgaag a 21

<210> 49
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 49
aaggaaaatg caggtgaaga c 21

<210> 50
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Sythesized Sequence

<400> 50
aaaatgcagg tgaagaccga g 21

<210> 51
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized sequence

<400> 51
aaatgcagggt gaagaccag g 21

<210> 52
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 52
aaagccaagg aagcagagat c 21

<210> 53
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthesized Sequence

 <400> 53
 aagccaagga agcagagatc c 21

 <210> 54
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthesized Sequence

 <400> 54
 aaggaagcag agatccagcc t 21

 <210> 55
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthesized Sequence

 <400> 55
 aagcagagat ccagccttct g 21

 <210> 56
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthesized Sequence

 <400> 56
 aaaaaggcct agacggagca a 21

 <210> 57
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthesized sequence

 <400> 57
 aaaaggccta gacggagcaa a 21

 <210> 58
 <211> 21
 <212> DNA

<213> Artificial
 <220>
 <223> Synthesized Sequence
 <400> 58
 aaaggcctag acggagcaaa a 21

 <210> 59
 <211> 21
 <212> DNA
 <213> Artificial
 <220>
 <223> Synthesized Sequence
 <400> 59
 aaggcctaga cggagcaaaa a 21

 <210> 60
 <211> 21
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35 40 45

Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val
50 55 60

Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn
65 70 75 80

Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser
85 90 95

Ala Gln Ser Gly Ala Gly Lys Leu Lys Ser Cys Asp Lys Pro His Thr
100 105 110

Cys Pro Leu Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
115 120 125

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
130 135 140

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
145 150 155 160

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
33

165

170

175

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
180 185 190

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
195 200 205

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
210 215 220

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
225 230 235 240

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
245 250 255

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
260 265 270

Gln Pro Glu Asn Asn Tyr Lys Ala Thr Pro Pro Val Leu Asp Ser Asp
275 280 285

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
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